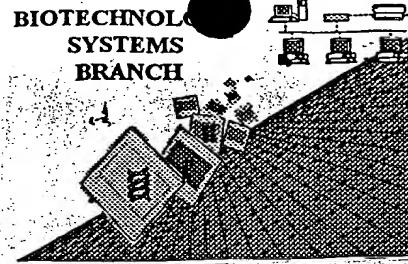


RAW SEQUENCE LISTING ERROR REPORT



7

B7

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/674,337

Source: PCT/09

Date Processed by STIC: 10/26/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/674,337

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFT

1 Wrapped Nucleic
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
 (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
 Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 Use of <220>

Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

Please
consult
Sequence Rules
Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Japan Science And Technology Corporation
6 <120> TITLE OF INVENTION: Nicotianamine synthase, genes coding nicotianamine synthase
8 <130> FILE REFERENCE: PA906235
10 <140> CURRENT APPLICATION NUMBER: US/09/674,337
10 <141> CURRENT FILING DATE: 2001-08-22
10 <160> NUMBER OF SEQ ID NOS: 22

ERRORED SEQUENCES

12 <210> SEQ ID NO: 1
13 <211> LENGTH: 328
14 <212> TYPE: PRT
15 <213> ORGANISM: Hordeum vulgare L.
OK-> 16 <400> SEQUENCE: 1
18 Met Asp Ala Gln Asn Lys Glu Val Ala Ala Leu Ile Glu Lys Ile
19 Ala Gly Ile Gln Ala Ala Ile Ala Glu Leu Pro Ser Leu Ser Pro
20 Ser Pro Glu Val Asp Arg Leu Phe Thr Asp Leu Val Thr Ala Cys
21 Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Ser Pro Glu His
22 Gln Arg Met Arg Glu Ala Leu Ile Arg Leu Cys Ser Ala Ala Glu
23 Gly Lys Leu Glu Ala His Tyr Ala Asp Leu Leu Ala Thr Phe Asp
24 Asn Pro Leu Asp His Leu Gly Leu Phe Pro Tyr Tyr Ser Asn Tyr
25 Val Asn Leu Ser Arg Leu Glu Tyr Glu Leu Leu Ala Arg His Val
26 Pro Gly Ile Ala Pro Ala Arg Val Ala Phe Val Gly Ser Gly Pro
27 Leu Pro Phe Ser Ser Leu Val Leu Ala Ala His His Leu Pro Glu
28 Thr Gln Phe Asp Asn Tyr Asp Leu Cys Gly Ala Ala Asn Glu Arg
29 Ala Arg Lys Leu Phe Gly Ala Thr Ala Asp Gly Val Gly Ala Arg
30 Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr Gln Glu Leu
31 Gly Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala
32 Ala Glu Glu Lys Ala Lys Val Ile Ala His Leu Gly Ala His Met
33 Val Glu Gly Ala Ser Leu Val Val Arg Ser Ala Arg Pro Arg Gly
34 Phe Leu Tyr Pro Ile Val Asp Pro Glu Asp Ile Arg Arg Gly Gly
35 Phe Glu Val Leu Ala Val His His Pro Glu Gly Glu Val Ile Asn
36 Ser Val Ile Val Ala Arg Lys Ala Val Glu Ala Gln Leu Ser Gly
37 Pro Gln Asn Gly Asp Ala His Ala Arg Gly Ala Val Pro Leu Val
38 Ser Pro Pro Cys Asn Phe Ser Thr Lys Met Glu Ala Ser Ala Leu
E--> 39 Glu Lys Ser Glu Glu Leu Thr Ala Lys Glu Leu Ala Phe
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 1295
44 <212> TYPE: DNA
45 <213> ORGANISM: Hordeum vulgare L.

W--> 46 <400> SEQUENCE: 2

E--> 47 10 20 30 40 50 60
E--> 48 gcttcagag gttccagag ttttccgggt caccaagaag catttgatca taacatggat 60
E--> 50 70 80 90 100 110 120
E--> 51 gcccagaaca aggaggtcgc tgctctgatc gagaagatcg ccggtatcca ggccggccatc 120
E--> 53 130 140 150 160 170 180

IMPORTANT: all bases MUST be in lower-case

letters when using new Sequence Rules format

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

E--> 54 gccgagctgc cgtcgctgag cccgtcccc gaggtcgaca ggctttcac cgacctcgct
E--> 56 ~~190~~ ~~200~~ ~~210~~ ~~220~~ ~~230~~ ~~240~~
E--> 57 acggcctcg cgccggcag cccgtcgac gtgacgaagc tcagccgga gcaccagagg
E--> 59 ~~250~~ ~~260~~ ~~270~~ ~~280~~ ~~290~~ ~~300~~
E--> 60 atgcgggagg ctctcatccg cttgtgtcc gccggcagg ggaagctcga ggcgcactac
E--> 62 ~~310~~ ~~320~~ ~~330~~ ~~340~~ ~~350~~ ~~360~~
E--> 63 gccgacacctc tcgccccctt cgacaacccg ctgcaccacc tcggccttcccgtactac
E--> 65 ~~370~~ ~~380~~ ~~390~~ ~~400~~ ~~410~~ ~~420~~
E--> 66 agcaactacg tcaacacctcg caggctggag tacgagctcc tggcgccca cgtggccggc
E--> 68 ~~430~~ ~~440~~ ~~450~~ ~~460~~ ~~470~~ ~~480~~
E--> 69 atcgcggcgg cgccgtcgcc ttctgtcgcc tccggccgc tgccgtttag ctgcgtcgct
E--> 71 ~~490~~ ~~500~~ ~~510~~ ~~520~~ ~~530~~ ~~540~~
E--> 72 ctgcggcgc accacacctcgcc cgagacccag ttgcacaact acgacacctgtg cggcgccggc
E--> 74 ~~550~~ ~~560~~ ~~570~~ ~~580~~ ~~590~~ ~~600~~
E--> 75 aacgagcgcg ccaggaagct ttccggcgcg acggcggacg gcttcggcgc gctatgtcg
E--> 77 ~~610~~ ~~620~~ ~~630~~ ~~640~~ ~~650~~ ~~660~~
E--> 78 ttcccacacgg cggacgtcgcc gacacctacc caggagctcg ggcctacga cgtgtcttc
E--> 80 ~~670~~ ~~680~~ ~~690~~ ~~700~~ ~~710~~ ~~720~~
E--> 81 ctgcggcgc tcgtcgccat ggcagccgag gagaaggcca aggtgattgc ccacccggc
E--> 83 ~~730~~ ~~740~~ ~~750~~ ~~760~~ ~~770~~ ~~780~~
E--> 84 ggcacatgg tggagggggc gtccctggtc gtgcggagcg cacggccccc cggctttctt
E--> 86 ~~790~~ ~~800~~ ~~810~~ ~~820~~ ~~830~~ ~~840~~
E--> 87 taccggattt tcgacccgga ggacatcagg cgggggtgggt tcgaggtgt ggcgtgcac
E--> 89 ~~850~~ ~~860~~ ~~870~~ ~~880~~ ~~890~~ ~~900~~
E--> 90 cacccggaaat gtgagggtat caactctgtc atcgtcgccc gtaaggccgt cgaagcgcag
E--> 92 ~~910~~ ~~920~~ ~~930~~ ~~940~~ ~~950~~ ~~960~~
E--> 93 ctcagtgggc cgccagaacgg agacgcgcac gcacggggcg cgggtccgtt ggtcagcccg
E--> 95 ~~970~~ ~~980~~ ~~990~~ ~~1000~~ ~~1010~~ ~~1020~~
E--> 96 ccatgcaact tctccaccaa gatggaggcg agcgcgtttg agaagagcga ggagctgacc
E--> 98 ~~1030~~ ~~1040~~ ~~1050~~ ~~1060~~ ~~1070~~ ~~1080~~
E--> 99 gccaaagacg tggcctttt attgaagagt ggcgtggtc attctgtcgct gtcgtatcg
E--> 101 ~~1090~~ ~~1100~~ ~~1110~~ ~~1120~~ ~~1130~~ ~~1140~~
E--> 102 ggttaactttc ctactctgtgt gtgtttttagt gtttgcct gtaagagtt tgcttccggc
E--> 104 ~~1150~~ ~~1160~~ ~~1170~~ ~~1180~~ ~~1190~~ ~~1200~~
E--> 105 cttgtgtgt taatttacac gctttacatg tagtacttgtt atttataacct ggaataacgg
E--> 107 ~~1210~~ ~~1220~~ ~~1230~~ ~~1240~~ ~~1250~~ ~~1260~~
E--> 108 tatgttaacat aaatatttagt gggattttagaa gtgttaatgtct aaataataag aaaactttagt
E--> 110 ~~1270~~ ~~1280~~ ~~1290~~ ~~1300~~
E--> 111 gcagacattc aaaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaa

114 <210> SEQ ID NO: 3

115 <211> LENGTH: 335

116 <212> TYPE: PRT

117 <213> ORGANISM: Hordeum vulgare L.

NC> 118 <400> SEQUENCE: 3

120 Met Ala Ala Gln Asn Asn Gln Glu Val Asp Ala Leu Val Glu Lys
121 Ile Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser
122 Pro Ser Pro Asp Val Asp Ala Leu Phe Thr Glu Leu Val Thr Ala
123 Cys Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Gly Pro Glu
124 Ala Gln Glu Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala

Please
insert
cumulative
base totals
at right
margin of
each line

same errors as Sequence 1

15
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

125 Glu Gly Lys Leu Glu Ala His Tyr Ser Asp Met Leu Ala Ala Phe
 126 Asp Lys Pro Leu Asp His Leu Gly Met Phe Pro Tyr Tyr Asn Asn
 127 Tyr Ile Asn Leu Ser Lys Leu Glu Tyr Glu Leu Leu Ala Arg Tyr
 128 Val Pro Gly Gly Tyr Arg Pro Ala Arg Val Ala Phe Ile Gly Ser
 129 Gly Pro Leu Pro Phe Ser Ser Phe Val Leu Ala Ala Arg His Leu
 130 Pro Asp Thr Met Phe Asp Asn Tyr Asp Leu Cys Gly Ala Ala Asn
 131 Asp Arg Ala Ser Lys Leu Phe Arg Ala Asp Arg Asp Val Gly Ala
 132 Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Ala Gly Glu
 133 Leu Ala Lys Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met
 134 Ala Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala His
 135 Met Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala His Gly Ala
 136 Arg Gly Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg
 137 Gly Gly Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val
 138 Val Asn Ser Val Ile Ile Ala Gln Lys Ser Lys Asp Val His Ala
 139 Asp Gly Leu Gly Ser Gly Arg Gly Ala Gly Gly Gln Tyr Ala Arg
 140 Gly Thr Val Pro Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met
 141 Val Ala Asp Val Thr Gln Asn His Lys Arg Asp Glu Phe Ala Asn

E--> 142 Ala Glu Val Ala Phe

145 <210> SEQ ID NO: 4

146 <211> LENGTH: 1342

147 <212> TYPE: DNA

148 <213> ORGANISM: Hordeum vulgare L.

W--> 149 <400> SEQUENCE: 4

E--> 151 10 20 30 40 50 60
 E--> 152 ctcctgtgcc tgcctgagg taccaagaac accagtggaaa tggctgccc gaacaaccag
 E--> 154 70 80 90 100 110 120
 E--> 155 gaggtggatg ccctgggtga gaagatcacc gggctccatg ccgcaatcgc caagctgccc
 E--> 157 130 140 150 160 170 180
 E--> 158 tcgctcagcc catccccggc cgtcgacgcg ctcttcacgg agctggtcac ggcgtgcgtt
 E--> 160 190 200 210 220 230 240
 E--> 161 ccaccgagtc cagtggacgt gaccaagctc gggccggagg cgcaggagat gcgggaggc
 E--> 163 250 260 270 280 290 300
 E--> 164 ctcatccgccc tatgctccga ggccgagggg aagctggagg cgcactactc cgacatgctc
 E--> 166 310 320 330 340 350 360
 E--> 167 gccgccttcg acaagccgct ggatcacctc ggcattttcc cctactacaa caactacatc
 E--> 169 370 380 390 400 410 420
 E--> 170 aacctcagca agctcgagta cgagctccgt gcccgtacg tgcctggcgg ctatcgcccg
 E--> 172 430 440 450 460 470 480
 E--> 173 ggcgcgtcg cgttcatcg ctccggcccg ctgcgttca gtcctttgt cctggccgc
 E--> 175 490 500 510 520 530 540
 E--> 176 cgccacactgc ccgacaccat ttgcacaaac tatgacctgt ggggtgcggc caacgatcgc
 E--> 178 550 560 570 580 590 600
 E--> 179 gccagcaagc tcttcgcgc ggatcgacgt gtgggtgccc gcatgtcggtt ccacacggcc
 E--> 181 610 620 630 640 650 660
 E--> 182 gacgtcgccg acctcgccgg cgagctcgcc aagtacgacg ttgtcttcgtt ggccgcactc
 E--> 184 670 680 690 700 710 720
 E--> 185 gtcggcatgg ccggcgagga caaggcgaag gtgatcgcc acctcgccgc acacatggca
 E--> 187 730 740 750 760 770 780
 E--> 188 gacggggcgg ccctcgctgt ggcagcgcac cagggagcgc ggggttctt gtacccgatc

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*invalid
numbering
follow directions
mp.1*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

E--> 190 790 800 810 820 830 840
E--> 191 gtcgacccccc aggacatcg 850 860 870 880 890 900
E--> 193 850 860 870 880 890 900
E--> 194 gacgacgtgg tgaactccgt catcatcgca cagaagtcca aggacgtgca tgccgatgga
E--> 196 910 920 930 940 950 960
E--> 197 cttggcagcg ggcgtggtgc cggtggacag tacgcgcgg gcacggtgcc tggatgc
E--> 199 970 980 990 1000 1010 1020
E--> 200 ccccccgtgca gggttcggcga gatggtggcg gacgtgaccc agaaccacaa gagagacgag
E--> 202 1030 1040 1050 1060 1070 1080
E--> 203 tttgccaacg ccgaagtggc cttttgatcg ttgcgtgcga ggggtgtcat ccatgatcca
E--> 205 1090 1100 1110 1120 1130 1140
E--> 206 tccatCACCTC gttctgtgat tgcatacaagc ttgcataatcg atgcatttca agtcacgtgt
E--> 208 1150 1160 1170 1180 1190 1200
E--> 209 tgcttctatc caataatgtt cgtgtgggt ttacacgcga atgtcttgcata gacctttgtt
E--> 211 1210 1220 1230 1240 1250 1260
E--> 212 tggatcacaag tgaattttaa ttccacaagta catataatgg tcaccattgtt aaagatgttt
E--> 214 1270 1280 1290 1300 1310 1320
E--> 215 agtgtgtgtt ttccaaatata tggttgcgtt aggttcatca tctaataaaaa tatgtttggaa
E--> 217 1330 1340 1350
E--> 218 accccaaaaaaa aaaaaaaaaaa aa

221 <210> SEQ ID NO: 5
222 <211> LENGTH: 335
223 <212> TYPE: PRT
224 <213> ORGANISM: Hordeum vulgare L.

W--> 225 <400> SEQUENCE: 5

227 Met Ala Ala Gln Asn Asn Asn Lys Asp Val Ala Ala Leu Val Glu
228 Lys Ile Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu
229 Ser Pro Ser Pro Asp Val Asp Ala Leu Phe Thr Glu Leu Val Thr
230 Ala Cys Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Gly Pro
231 Glu Ala Gln Glu Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu
232 Ala Glu Gly Lys Leu Glu Ala His Tyr Ser Asp Met Leu Ala Ala
233 Phe Asp Asn Pro Leu Asp His Leu Gly Ile Phe Pro Tyr Tyr Ser
234 Asn Tyr Ile Asn Leu Ser Lys Leu Glu Tyr Glu Leu Leu Ala Arg
235 Tyr Val Arg Arg His Arg Pro Ala Arg Val Ala Phe Ile Gly Ser
236 Gly Pro Leu Pro Phe Ser Ser Phe Val Leu Ala Ala Arg His Leu
237 Pro Asp Thr Met Phe Asp Asn Tyr Asp Leu Cys Gly Ala Ala Asn
238 Asp Arg Ala Ser Lys Leu Phe Arg Ala Asp Thr Asp Val Gly Ala
239 Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Ala Ser Glu
240 Leu Ala Lys Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met
241 Ala Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala His
242 Met Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala His Gly Ala
243 Arg Gly Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg
244 Gly Gly Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val
245 Val Asn Ser Val Ile Ile Ala Gln Lys Ser Lys Glu Val His Ala
246 Asp Gly Leu Gly Ser Ala Arg Gly Ala Gly Arg Gln Tyr Ala Arg
247 Gly Thr Val Pro Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met
248 Val Ala Asp Val Thr Gln Asn His Lys Arg Asp Glu Phe Ala Asn
E--> 249 Ala Glu Val Ala Phe

252 <210> SEQ ID NO: 6

*same
err*

same err or p.1

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

253 <211> LENGTH: 1314
254 <212> TYPE: DNA
255 <213> ORGANISM: Hordeum vulgare L.
W--> 256 <400> SEQUENCE: 6

E--> 257	10	20	30	40	50	60
E--> 258	ctacttca	cacactagt	cccagaaaga	aggctgcaat	ggctgcccag	aacaacaaca
E--> 260	70	80	90	100	110	120
E--> 261	aggatgtcgc	tgccctgg	gagaagatca	ccgggctcca	cgccgc	ccatc gccaagctgc
E--> 263	130	140	150	160	170	180
E--> 264	cgtcgctc	agcccc	gacgtcgac	cgctt	cgactgtgc	acggcgtcg
E--> 266	190	200	210	220	230	240
E--> 267	ttcccc	ccccgtgg	gtgaccaag	tcggcccc	ggcgcaggag	atgcgggagg
E--> 269	250	260	270	280	290	300
E--> 270	gcctcatcc	cctctgctcc	gaggccgagg	ggaagctgg	ggcgcactac	tccgacatgc
E--> 272	310	320	330	340	350	360
E--> 273	tcgccc	cgtt	cgacaaccc	ctggatcacc	tcggcatctt	cccctactac agcaactaca
E--> 275	370	380	390	400	410	420
E--> 276	tcaac	tcag	caagctgg	tacgagctcc	tggcacgct	cgtccggcgg catcgccgg
E--> 278	430	440	450	460	470	480
E--> 279	cccg	cg	gttcatcg	gc	tccggcc	tc tgccgttc
E--> 281	490	500	510	520	530	540
E--> 282	gccac	ctg	cg	cgacaccat	tttgacaa	acgac
E--> 284	550	560	570	580	590	600
E--> 285	ccagca	agct	cttcc	cg	gacacgg	tggtgccc
E--> 287	610	620	630	640	650	660
E--> 288	acgt	cg	cg	gag	ctcgcc	actacgac
E--> 290	670	680	690	700	710	720
E--> 291	tcgg	catgg	gc	cg	cc	cg aaggcca
E--> 293	730	740	750	760	770	780
E--> 294	acgggg	cg	cc	tcgtc	gtcg	cgac
E--> 296	790	800	810	820	830	840
E--> 297	tcgac	cccc	ca	ggacatcg	cg	cgccgggt
E--> 299	850	860	870	880	890	900
E--> 300	acgac	gtgg	gt	gactcc	atc	atcgac
E--> 302	910	920	930	940	950	960
E--> 303	ttgg	cag	gc	gtgt	gt	gc
E--> 305	970	980	990	1000	1010	1020
E--> 306	cccc	gtc	g	ttcggt	g	atggtgg
E--> 308	1030	1040	1050	1060	1070	1080
E--> 309	ttg	cca	ac	gtgg	tcgt	ccaa
E--> 311	1090	1100	1110	1120	1130	1140
E--> 312	atgt	ggtag	gt	atgttgc	tac	tcgtcgt
E--> 314	1150	1160	1170	1180	1190	1200
E--> 315	ctact	acc	gc	tgttat	tttca	aggca
E--> 317	1210	1220	1230	1240	1250	1260
E--> 318	agg	gtt	aca	cg	ca	ttacac
E--> 320	1270	1280	1290	1300	1310	1320
E--> 321	cag	ttc	aca	aa	aaa	aaaaaaa
324	<210>	SEQ	ID	NO:	7	

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

325 <211> LENGTH: 329

326 <212> TYPE: PRT

327 <213> ORGANISM: Hordeum vulgare L.

W--> 328 <400> SEQUENCE: 7

330	Met	Asp	Gly	Gln	Ser	Glu	Glu	Val	Asp	Ala	Leu	Val	Gln	Lys	Ile	15
331	Thr	Gly	Leu	His	Ala	Ala	Ile	Ala	Lys	Leu	Pro	Ser	Leu	Ser	Pro	30
332	Ser	Pro	Asp	Val	Asp	Ala	Leu	Phe	Thr	Asp	Leu	Val	Thr	Ala	Cys	45
333	Val	Pro	Pro	Ser	Pro	Val	Asp	Val	Thr	Lys	Leu	Ala	Pro	Glu	Ala	60
334	Gln	Ala	Met	Arg	Glu	Gly	Leu	Ile	Arg	Leu	Cys	Ser	Glu	Ala	Glu	75
335	Gly	Lys	Leu	Glu	Ala	His	Tyr	Ser	Asp	Met	Leu	Ala	Ala	Phe	Asp	90
336	Asn	Pro	Leu	Asp	His	Leu	Gly	Val	Phe	Pro	Tyr	Tyr	Ser	Asn	Tyr	105
337	Ile	Asn	Leu	Ser	Lys	Leu	Glu	Tyr	Glu	Leu	Ala	Arg	Tyr	Val	120	
338	Pro	Gly	Arg	His	Arg	Pro	Ala	Arg	Val	Ala	Phe	Ile	Gly	Ser	Gly	135
339	Pro	Leu	Pro	Phe	Ser	Ser	Tyr	Val	Leu	Ala	Ala	Arg	His	Leu	Pro	150
340	Asp	Thr	Val	Phe	Asp	Asn	Tyr	Asp	Leu	Cys	Gly	Ala	Ala	Asn	Asp	165
341	Arg	Ala	Thr	Arg	Leu	Phe	Arg	Ala	Asp	Lys	Asp	Val	Gly	Ala	Arg	180
342	Met	Ser	Phe	His	Thr	Ala	Asp	Val	Ala	Asp	Leu	Thr	Asp	Glu	Leu	195
343	Ala	Thr	Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Ala	210
344	Ala	Glu	Asp	Lys	Ala	Lys	Val	Ile	Ala	His	Leu	Gly	Ala	His	Met	225
345	Ala	Asp	Gly	Ala	Ala	Leu	Val	Ala	Arg	His	Gly	Ala	Arg	Gly	Phe	240
346	Leu	Tyr	Pro	Ile	Val	Asp	Pro	Gln	Asp	Ile	Gly	Arg	Gly	Gly	Phe	255
347	Glu	Val	Leu	Ala	Val	Cys	His	Pro	Asp	Asp	Asp	Val	Val	Asn	Ser	270
348	Val	Ile	Ile	Ala	Gln	Lys	Ser	Asn	Asp	Val	His	Glu	Tyr	Gly	Leu	285
349	Gly	Ser	Gly	Arg	Gly	Gly	Arg	Tyr	Ala	Arg	Gly	Thr	Val	Val	Pro	300
350	Val	Val	Ser	Pro	Pro	Cys	Arg	Phe	Gly	Glu	Met	Val	Ala	Asp	Val	315

E--> 351 Thr Gln Lys Arg Glu Glu Phe Ala Asn Ala Glu Val Ala Phe

unpublished
no S

353 <210> SEQ ID NO: 8

354 <211> LENGTH: 1249

355 <212> TYPE: DNA

356 <213> ORGANISM: Hordeum vulgare L.

W--> 357 <400> SEQUENCE: 8

E--> 359	10	20	30	40	50	60
E--> 360	ccactaccga	ctaccgtagt	accgtgcctc	agagctcatc	actggtcagg	taccaagaag
E--> 362	70	80	90	100	110	120
E--> 363	acataaaaat	ggacggccag	agcgaggagg	tcgacgcct	tgtccagaag	atcaccggcc
E--> 365	130	140	150	160	170	180
E--> 366	tccacgcccgc	catcgccaag	ctgcccctcgc	tcagccccgtc	cccgacgtc	gacgcgtct
E--> 368	190	200	210	220	230	240
E--> 369	tcacccgacct	ggtcacccgcg	tgcggtcccc	cgagcccccgt	ggacgtgacc	aagctcgccc
E--> 371	250	260	270	280	290	300
E--> 372	cggaggcgca	ggcgatgcgg	gagggcctca	tccgcctctg	ctccgaggcc	gagggcaagc
E--> 374	310	320	330	340	350	360
E--> 375	tggaggcgca	ctactccgac	atgctcgccg	ccttcgacaa	cccgctcgac	cacctcgccg
E--> 377	370	380	390	400	410	420
E--> 378	tcttccctca	ctacagcaac	tacatcaacc	tcagcaagct	tgagtacgag	ctcctcgcc
E--> 380	430	440	450	460	470	480
E--> 381	gctacgtgcc	ccgcaggcat	cgcccgccccc	gcgtgcgcctt	catcggtcc	ggcccgctgc
E--> 383	490	500	510	520	530	540
E--> 384	cgttcagctc	ctacgtcctc	gccgcgcgcc	acctgcccga	caccgtttc	gacaactacg

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674, 337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

E--> 386 550 560 570 580 590 600
E--> 387 acctgtgcgg cgccggccaac gaccgcgcga ccaggctgtt ccgcgcggac aaggacgtcg
E--> 389 610 620 630 640 650 660
E--> 390 gcgcccgcac gtcgttccac accgcccacg tcgcggacct caccgacgag ctgcgtacgt
E--> 392 670 680 690 700 710 720
E--> 393 acgacgtcgt cttcctggcc gcgctcggtt gcatggccgc cgaggacaag gccaagggtga
E--> 395 730 740 750 760 770 780
E--> 396 tcgcgcaccc tggcgcgcac atggcggacg gggcggccct cggtgcgcgg cacggcgcgc
E--> 398 790 800 810 820 830 840
E--> 399 gtgggttcct ctacccgatc gtcgatcccc aggacatcggtt cgaggcggg ttcgagggtgc
E--> 401 850 860 870 880 890 900
E--> 402 tcgcccgtgt tcaccccgac gacgacgtgg tgaactccgt catcatcgca caaaagagca
E--> 404 910 920 930 940 950 960
E--> 405 acgacgtgca cgagtatgga cttggcagcg ggcgtgggtt acggtaacgcg cgaggcacgg
E--> 407 970 980 990 1000 1010 1020
E--> 408 tgggtcccggtt ggtcagccca ccctgcaggt tcggcgagat ggtggcagac gtgaccaga
E--> 410 1030 1040 1050 1060 1070 1080
E--> 411 agagagagga gtttgcac gcgaaagtgg ctttctgatt gctgctgaat cgcttgtgat
E--> 413 1090 1100 1110 1120 1130 1140
E--> 414 cgtacgtgtt aattttctta ctactcctcc tcctaccacc acctatcacc tatgtatgca
E--> 416 1150 1160 1170 1180 1190 1200
E--> 417 tttcaagtgcg tgggtgtttt gtatccaata atgtaagtga gatgtttaca cgcgcaaaaa
E--> 419 1210 1220 1230 1240 1250
E--> 420 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa
423 <210> SEQ ID NO: 9
424 <211> LENGTH: 282
425 <212> TYPE: PRT
426 <213> ORGANISM: Hordeum vulgare L.

W--> 427 <400> SEQUENCE: 9

429	Met	Glu	Ala	Glu	Asn	Gly	Glu	Val	Ala	Ala	Leu	Val	Glu	Lys	Ile	15
430	Thr	Gly	Leu	His	Ala	Ala	Ile	Ser	Lys	Leu	Pro	Ala	Leu	Ser	Pro	30
431	Ser	Pro	Gln	Val	Asp	Ala	Leu	Phe	Thr	Glu	Leu	Val	Ala	Ala	Cys	45
432	Val	Pro	Ser	Ser	Pro	Val	Asp	Val	Thr	Lys	Leu	Gly	Pro	Glu	Ala	60
433	Gln	Glu	Met	Arg	Gln	Asp	Leu	Ile	Arg	Leu	Cys	Ser	Ala	Ala	Glu	75
434	Gly	Leu	Leu	Glu	Ala	His	Tyr	Ser	Asp	Met	Leu	Thr	Ala	Leu	Asp	90
435	Ser	Pro	Leu	Asp	His	Leu	Gly	Arg	Phe	Pro	Tyr	Phe	Asp	Asn	Tyr	105
436	Val	Asn	Leu	Ser	Lys	Leu	Glu	His	Asp	Leu	Leu	Ala	Gly	His	Val	120
437	Ala	Ala	Pro	Ala	Arg	Val	Ala	Phe	Ile	Gly	Ser	Gly	Pro	Leu	Pro	135
438	Phe	Ser	Ser	Leu	Phe	Leu	Ala	Thr	Tyr	His	Leu	Pro	Asp	Thr	Arg	150
439	Phe	Asp	Asn	Tyr	Asp	Arg	Cys	Ser	Val	Ala	Asn	Gly	Arg	Ala	Met	165
440	Lys	Leu	Val	Gly	Ala	Ala	Asp	Glu	Gly	Val	Arg	Ser	Arg	Met	Ala	180
441	Phe	His	Thr	Ala	Glu	Val	Thr	Asp	Leu	Thr	Ala	Glu	Leu	Gly	Ala	195
442	Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Thr	Ser	Lys	210
443	Glu	Lys	Ala	Asp	Ala	Ile	Ala	His	Leu	Gly	Lys	His	Met	Ala	Asp	225
444	Gly	Ala	Val	Leu	Val	Arg	Glu	Ala	Leu	His	Gly	Ala	Arg	Ala	Phe	240
445	Leu	Tyr	Pro	Val	Val	Glu	Leu	Asp	Asp	Val	Gly	Arg	Gly	Gly	Phe	255
446	Gln	Val	Leu	Ala	Val	His	His	Pro	Ala	Gly	Asp	Glu	Val	Phe	Asn	270
E--> 447	Ser	Phe	Ile	Val	Ala	Arg	Lys	Val	Lys	Met	Ser	Ala				282
449	<210>	SEQ	ID	NO:	10											

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

450 <211> LENGTH: 1044
 451 <212> TYPE: DNA
 452 <213> ORGANISM: Hordeum vulgare L.
 W--> 453 <400> SEQUENCE: 10
 E--> 455 10 20 30 40 50 60
 E--> 456 gtgacatgga ggccgaaaac ggcgagggtgg ctgctctggc cgagaagatc accggctctcc
 E--> 458 70 80 90 100 110 120
 E--> 459 acgcccattt ctccaagctc ccggcactaa gcccgtctcc tcaagtcgac ggcgttca
 E--> 461 130 140 150 160 170 180
 E--> 462 ccgagctggc tgcggcgtgc gtcccatcaa gcccgtggc cgtgaccaag ctggccgg
 E--> 464 190 200 210 220 230 240
 E--> 465 aggccgcagg gatgcggcag gacccatcc gtctctgctc ggccgcccgg gggctgctcg
 E--> 467 250 260 270 280 290 300
 E--> 468 aggccgcacta ctccgacatg ctcaccgcgt tggacagccc gctcgaccac ctggccgc
 E--> 470 310 320 330 340 350 360
 E--> 471 tcccttactt cgacaactac gtcaacccatca gcaagctcga gcacgatctt ctggcaggc
 E--> 473 370 380 390 400 410 420
 E--> 474 acgtggcggc cccggccgcgtc ttggcgttca tcgggtcggg gccactggc ttcagctgc
 E--> 476 430 440 450 460 470 480
 E--> 477 tcttccttgc gacgtaccac ctgcccggaca cccgggttca caactacgac cgggtcagcg
 E--> 479 490 500 510 520 530 540
 E--> 480 tggcgaatgg ccggggcgtg aagctggcgtc ggcggccggc cgagggcgtg cgatcacgca
 E--> 482 550 560 570 580 590 600
 E--> 483 tggcgttcca cacggccgaa gtcacggacc tcacggctga gctcggcgct tacgacgtgg
 E--> 485 610 620 630 640 650 660
 E--> 486 tcttccttgc cgcgtcgtg ggaatgacgt ccaaggagaa ggccgacgcc atagcgcact
 E--> 488 670 680 690 700 710 720
 E--> 489 tggggaaagca catggcagat gggggcgggtgc tcgtgcgcga agcgctgcac gggggcgcgag
 E--> 491 730 740 750 760 770 780
 E--> 492 cgttccttgc tcctgtcgtg gagctggacg atgtcgccggc tgggtgggttc caagtgcgtgg
 E--> 494 790 800 810 820 830 840
 E--> 495 ccgtgcacca ccctgcaggc gatgagggtgt tcaactcatt catagttgcc cggaagggtga
 E--> 497 850 860 870 880 890 900
 E--> 498 aaatgagtgc tttaaattaaag aaaagggtga gcctgtctgc ttgtgcaaat ggtgtctcac
 E--> 500 910 920 930 940 950 960
 E--> 501 attgataata accagatgat accctgcaca ttgtatgggg tactgcagta tgtttcaatg
 E--> 503 970 980 990 1000 1010 1020
 E--> 504 aggtctgggt gtatcaaata tgagtatttgc tttaataat atcagcgaat atgtttcgat
 E--> 506 1030 1040 1050
 E--> 507aaaaaaaaaaaaaaa
 509 <210> SEQ ID NO: 11
 510 <211> LENGTH: 328
 511 <212> TYPE: PRT
 512 <213> ORGANISM: Hordeum vulgare L.
 W--> 513 <400> SEQUENCE: 11
 515 Met Asp Ala Gln Asn Lys Glu Val Asp Ala Leu Val Gln Lys Ile 15
 516 Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro 30
 517 Ser Pro Asp Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys 45
 518 Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Gly Ser Glu Ala 60

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

519	Gln	Glu	Met	Arg	Glu	Gly	Leu	Ile	Arg	Leu	Cys	Ser	Glu	Ala	Glu	75
520	Gly	Lys	Leu	Glu	Ala	His	Tyr	Ser	Asp	Met	Leu	Ala	Ala	Phe	Asp	90
521	Asn	Pro	Leu	Asp	His	Leu	Gly	Met	Phe	Pro	Tyr	Tyr	Ser	Asn	Tyr	105
522	Ile	Asn	Leu	Ser	Lys	Leu	Glu	Tyr	Glu	Leu	Leu	Ala	Arg	Tyr	Val	120
523	Pro	Gly	Gly	Ile	Ala	Arg	Pro	Ala	Val	Ala	Phe	Ile	Gly	Ser	Gly	135
524	Pro	Leu	Pro	Phe	Ser	Ser	Tyr	Val	Leu	Ala	Ala	Arg	His	Leu	Pro	150
525	Asp	Ala	Met	Phe	Asp	Asn	Tyr	Asp	Leu	Cys	Ser	Ala	Ala	Asn	Asp	165
526	Arg	Ala	Ser	Lys	Leu	Phe	Arg	Ala	Asp	Lys	Asp	Val	Gly	Ala	Arg	180
527	Met	Ser	Phe	His	Thr	Ala	Asp	Val	Ala	Asp	Leu	Thr	Arg	Glu	Leu	195
528	Ala	Ala	Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Ala	210
529	Ala	Glu	Asp	Lys	Ala	Lys	Val	Ile	Pro	His	Leu	Gly	Ala	His	Met	225
530	Ala	Asp	Gly	Ala	Ala	Leu	Val	Val	Arg	Ser	Ala	Gln	Ala	Arg	Gly	240
531	Phe	Leu	Tyr	Pro	Ile	Val	Asp	Pro	Gln	Asp	Ile	Gly	Arg	Gly	Gly	255
532	Phe	Glu	Val	Leu	Ala	Val	Cys	His	Pro	Asp	Asp	Asp	Val	Val	Asn	270
533	Ser	Val	Ile	Ile	Ala	His	Lys	Ser	Lys	Asp	Val	His	Ala	Asn	Glu	285
534	Arg	Pro	Asn	Gly	Arg	Gly	Gly	Gln	Tyr	Arg	Gly	Ala	Val	Pro	Val	300
535	Val	Ser	Pro	Pro	Cys	Arg	Phe	Gly	Glu	Met	Val	Ala	Asp	Val	Thr	315
E-->	536	His	Lys	Arg	Glu	Glu	Phe	Thr	Asn	Ala	Glu	Val	Ala	Phe		328

539 <210> SEQ ID NO: 12

540 <211> LENGTH: 1352

541 <212> TYPE: DNA

542 <213> ORGANISM: Hordeum vulgare L.

W--> 543 <400> SEQUENCE: 12

E-->	545	10	20	30	40	50	60
E-->	546	ctccacttcg	ctcctgtgcc	tcaggtagcc	acaacataca	gtattaaaat	ggatgcccag
E-->	548	70	80	90	100	110	120
E-->	549	aacaaggagg	ttgatgccct	ggtccagaag	atcaccggcc	tccacgcccgc	catcgccaag
E-->	551	130	140	150	160	170	180
E-->	552	ctgcccgtccc	tcagcccatc	acccgacgtc	gacgcgtct	tcaccgacact	ggtcaccgcg
E-->	554	190	200	210	220	230	240
E-->	555	tgcgtccccc	cgagccccgt	ggacgtgacc	aagctcggt	cgaggcgca	ggagatgcgg
E-->	557	250	260	270	280	290	300
E-->	558	gagggcctca	tccgcctctg	ctccgaggcc	gaggggaagc	tggaggcgca	ctactccgac
E-->	560	310	320	330	340	350	360
E-->	561	atgctggccg	ctttcgacaa	cccgctcgac	cacctcgca	tgttccctta	ctacagcaac
E-->	563	370	380	390	400	410	420
E-->	564	tacatcaacc	tcagcaagct	ggagtacgag	ctccctggcgc	gctacgtgcc	ggggggcata
E-->	566	430	440	450	460	470	480
E-->	567	gccccggcccg	ctgtcgcgtt	catcggtccc	ggcccgctgc	cgttcagctc	ctacgtccctc
E-->	569	490	500	510	520	530	540
E-->	570	gccgctcgcc	acctgcccga	cgccatgttc	gacaactacg	acctgtgtag	cgccggcaac
E-->	572	550	560	570	580	590	600
E-->	573	gaccgtgcga	gcaagctgtt	ccgcgcggac	aaggacgtgg	gcccggcat	gtctttccac
E-->	575	610	620	630	640	650	660
E-->	576	accggccgacg	tagcggacact	cacccgcgag	ctcgccgcgt	acgacgtcgt	tttccctggcc
E-->	578	670	680	690	700	710	720
E-->	579	gcgctcgtgg	gcatggctgc	cgaggacaag	gccaagggtga	ttccgcacct	cgccgcgcac
E-->	581	730	740	750	760	770	780
E-->	582	atggcggacg	gggcggccct	cgtcgtgcgc	agtgcgcagg	cacgtgggtt	cctctacccg

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

E--> 584 790 800 810 820 830 840
E--> 585 atcgatcgatc cccaggacat cggatcgaggc gggtttgagg tgctggccgt gtgtcacc
E--> 587 850 860 870 880 890 900
E--> 588 gacgatgacg tggtaactc cgtcatcatc gcacacaagt ccaaggacgt gcatgcaat
E--> 590 910 920 930 940 950 960
E--> 591 gaacgtccca acgggcgtgg tggacagtac cggggcgcgg taccgggtgt cagccgcgg
E--> 593 970 980 990 1000 1010 1020
E--> 594 tgcagggtcg gtgagatggt ggcggacgtg acccacaaga gagaggagtt caccaacgcg
E--> 596 1030 1040 1050 1060 1070 1080
E--> 597 gaagtggcct tctgatcggtt gcgaggaaat gaaaatgaag gtggacgtgt gtggtcagca
E--> 599 1090 1100 1110 1120 1130 1140
E--> 600 tccatacgtg gctgcctgct tcatacgctt caatcgtaact actacctacc tatgcagttc
E--> 602 1150 1160 1170 1180 1190 1200
E--> 603 aagtcatgtg ttgtcaatgt aagtgtgtat tttacactag tctatgaaag gcagggcaga
E--> 605 1210 1220 1230 1240 1250 1260
E--> 606 cgagggtagt gtgccaagta acagtgtgtc attataggtg taagtgttga gaataagacc
E--> 608 1270 1280 1290 1300 1310 1320
E--> 609 atttttgttc acaaataatgtat tgatgtaaatc ggtgtcatat tcgtattttag tacatttgc
E--> 611 1330 1340 1350 1360
E--> 612 aagttgggttg ctaaaaaaaaaaaaaaa aa
615 <210> SEQ ID NO: 13
616 <211> LENGTH: 329
617 <212> TYPE: PRT
618 <213> ORGANISM: Hordeum vulgare L.

W--> 619 <400> SEQUENCE: 13

621 Met Asp Ala Gln Ser Lys Glu Val Asp Ala Leu Val Gln Lys Ile	15
622 Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro	30
623 Ser Pro Asp Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys	45
624 Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Ala Pro Glu Ala	60
625 Gln Ala Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu	75
626 Gly Lys Leu Glu Ala His Tyr Ser Asp Met Leu Ala Ala Phe Asp	90
627 Asn Pro Leu Asp His Leu Gly Val Phe Pro Tyr Tyr Ser Asn Tyr	105
628 Ile Asn Leu Ser Lys Leu Glu Tyr Glu Leu Leu Ala Arg Tyr Val	120
629 Pro Gly Gly Ile Ala Pro Ala Arg Val Ala Phe Ile Gly Ser Gly	135
630 Pro Leu Pro Phe Ser Ser Tyr Val Leu Ala Ala Arg His Leu Pro	150
631 Asp Thr Val Phe Asp Asn Tyr Val Pro Val Arg Ala Ala Asn Asp	165
632 Arg Ala Thr Arg Leu Phe Arg Ala Asp Lys Asp Val Gly Ala Arg	180
633 Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr Asp Glu Leu	195
634 Ala Thr Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala	210
635 Ala Glu Asp Lys Gly Gln Gly Asp Pro His Leu Gly Ala His Met	225
636 Ala Asp Gly Ala Ala Leu Val Arg Ser Ala His Gly Ala Arg Gly	240
637 Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly Gly	255
638 Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn	270
639 Ser Val Ile Ile Ala Gln Lys Ser Lys Asp Met Phe Ala Asn Gly	285
640 Pro Arg Asn Gly Cys Gly Gly Arg Tyr Ala Arg Gly Thr Val Pro	300
641 Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met Val Ala Asp Val	315
E--> 642 Thr Gln Lys Arg Glu Glu Phe Ala Lys Ala Glu Val Ala Phe	329
646 <210> SEQ ID NO: 14	
647 <211> LENGTH: 1371	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

648 <212> TYPE: DNA
649 <213> ORGANISM: Hordeum vulgare L.
W--> 650 <400> SEQUENCE: 14

	10	20	30	40	50
E--> 652	ggagcggnac	gcgtggcga	ggtgggcact	accgttagtac	cgtgcctcag
E--> 653	60	70	80	90	100
E--> 654	agctcatcac	tggtcaggta	ccaagaagac	ataaaaaatgg	acgcccagag
E--> 655	110	120	130	140	150
E--> 656	caaggaggtc	gacgcccttg	tccagaagat	caccggcctc	cacgcccggca
E--> 657	160	170	180	190	200
E--> 658	tcgccaagct	gccctcgctc	agccctgtccc	cggacgtcga	cgcgccttc
E--> 659	210	220	230	240	250
E--> 660	accgacacctgg	tcaccgcgtg	cgtgcccccg	agccccgtgg	acgtgaccaa
E--> 661	260	270	280	290	300
E--> 662	gctcgccccg	gaggcgcgagg	cgatgcggga	gggcctcata	cgcctctgtct
E--> 663	310	320	330	340	350
E--> 664	ccgaggccga	gggcaagctg	gaggcgact	actccgacat	gctcgccggcc
E--> 665	360	370	380	390	400
E--> 666	ttcgacaacc	cgctcgacca	cctcgccgtc	ttccccctact	acagcaacta
E--> 667	410	420	430	440	450
E--> 668	catcaacctc	agcaagctcg	agtacgagct	cctcgccgc	tacgtgccccg
E--> 669	460	470	480	490	500
E--> 670	gcggcatacg	cccgccccgc	gtcgccttca	tcggctccgg	ccgcctcccg
E--> 671	510	520	530	540	550
E--> 672	ttcagctcct	acgtcctcg	cgcgcgccac	ctgcccgaca	ccgtgttca
E--> 673	560	570	580	590	600
E--> 674	caactacgt	cctgtgcgcg	cggccaaacga	ccgcgcgacc	aggctgttcc
E--> 675	610	620	630	640	650
E--> 676	gcfgggacaaa	ggacgtcgcc	gcccgcacgt	cgttccacac	cgcgcacgtc
E--> 677	660	670	680	690	700
E--> 678	gcggacacta	ccgacgagct	cgctacgtac	gacgtcgct	tcctggccgc
E--> 679	710	720	730	740	750
E--> 680	gctcggtggc	atggccgccc	aggacaaggg	ccaaggtgat	ccgcacaccc
E--> 681	760	770	780	790	800
E--> 682	gcfgcgcacat	ggcggacggg	gccccctcg	tccgcagcgc	gcacggggcg
E--> 683	810	820	830	840	850
E--> 684	cgtgggttcc	tctacccgt	cgtcgatccc	caagacattg	gtcgaggcgg
E--> 685	860	870	880	890	900
E--> 686	gttcgaggtg	ctcgccgtgt	gtcaccggca	cgacgacgt	gtgaactccg
E--> 687	910	920	930	940	950
E--> 688	tcatcatcg	gcagaagtct	aaggacatgt	ttgccaatgg	acctcgcaac
E--> 689	960	970	980	990	1000
E--> 690	gggtgtggtg	gacgggtacgc	gcgaggcacg	gtgcccgtgg	tcagccggcc
E--> 691	1010	1020	1030	1040	1050
E--> 692	ctgcagggttc	ggcgagatgg	tggcagacgt	gaccgcagaag	agagaggagt
E--> 693	1060	1070	1080	1090	1100
E--> 694	ttgccaaggc	ggaagtggcc	ttctgattgc	tgcgagggtca	ccatccgtat
E--> 695	1110	1120	1130	1140	1150
E--> 696	gccgctgcta	ccttcaata	tcttcaata	gtaggtggcg	atttcctac

) also, see
item 9 on
Error Summary
Sheet

unrelated
n.s.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

E--> 698 1160 1170 1180 1190 1200
E--> 699 tcttgttacg acctttcaaa tcatatgttg tttgtaccca ataatgtaaag
E--> 700 1210 1220 1230 1240 1250
E--> 701 tgtgttgctt acacgcgcatt gtcttgcata ctcggtctct agaaggcagg
E--> 702 1260 1270 1280 1290 1300
E--> 703 gcagatcaag agactgtgca aaggaaaaga aatgtgtttt gttgttaggtg
E--> 704 1310 1320 1330 1340 1350
E--> 705 tatgagttgg gagtaagatg attctagttc aaaaaaaaaa aaaaaaaaaa
E--> 706 1360 1370 1380
E--> 707 aaaaaaaaaa aaaaaaaaaa a

711 <210> SEQ ID NO: 15

712 <211> LENGTH: 332

713 <212> TYPE: PRT

714 <213> ORGANISM: Oryza sativa L.

W--> 715 <400> SEQUENCE: 15

717 Met Glu Ala Gln Asn Gln Glu Val Ala Ala Leu Val Glu Lys lle 15
718 Ala Gly Leu His Ala Ala lle Ser Lys Leu Pro Ser Leu Ser Pro 30
719 Ser Ala Glu Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys 45
720 Val Pro Ala Ser Pro Val Asp Val Ala Lys Leu Gly Pro Glu Ala 60
721 Gln Ala Met Arg Glu Glu Leu lle Arg Leu Cys Ser Ala Ala Glu 75
722 Gly His Leu Glu Ala His Tyr Ala Asp Met Leu Ala Ala Phe Asp 90
723 Asn Pro Leu Asp His Leu Ala Arg Phe Pro Tyr Tyr Gly Asn Tyr 105
724 Val Asn Leu Ser Lys Leu Glu Tyr Asp Leu Leu Val Arg Tyr Val 120
725 Pro Gly lle Ala Pro Thr Arg Val Ala Phe Val Gly Ser Gly Pro 135
726 Leu Pro Phe Ser Ser Leu Val Leu Ala Ala His His Leu Pro Asp 150
727 Ala Val Phe Asp Asn Tyr Asp Arg Cys Gly Ala Ala Asn Glu Arg 165
728 Ala Arg Arg Leu Phe Arg Gly Ala Asp Glu Gly Leu Gly Ala Arg 180
729 Met Ala Phe His Thr Ala Asp Val Ala Thr Leu Thr Gly Glu Leu 195
730 Gly Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala 210
731 Ala Glu Glu Lys Ala Gly Val lle Ala His Leu Gly Ala His Met 225
732 Ala Asp Gly Ala Ala Leu Val Val Arg Thr Ala His Gly Ala Arg 240
733 Gly Phe Leu Tyr Pro lle Val Asp Pro Glu Asp Val Arg Arg Gly 255
734 Gly Phe Asp Val Leu Ala Val Cys His Pro Glu Asp Glu Val lle 270
735 Asn Ser Val lle Val Ala Arg Lys Val Gly Ala Ala Ala Ala Ala 285
736 Ala Ala Ala Arg Arg Asp Glu Leu Ala Asp Ser Arg Gly Val Val 300
737 Leu Pro Val Val Gly Pro Pro Ser Thr Cys Cys Lys Val Glu Ala 315
738 Ser Ala Val Glu Lys Ala Glu Glu Phe Ala Ala Asn Lys Glu Leu 330
E--> 739 Ser Val* *delete this* 345

741 <210> SEQ ID NO: 16

742 <211> LENGTH: 1372

743 <212> TYPE: DNA

744 <213> ORGANISM: Oryza sativa L.

746 <400> SEQUENCE: 16

E--> 750 10 20 30 40 50
E--> 751 ctccatTTgg ttgtcatttt caactataat ccaccacaac tcgtgcaaca
E--> 752 60 70 80 90 100
E--> 753 tcagctcact cgtgttccca accgcgcacaa agcttcacag atggaggctc
E--> 754 110 120 130 140 150
E--> 755 agaaccaaga ggtcgctgcc ctggtcgaga agatcgccgg cctccacgccc

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

E--> 756	160	170	180	190	200
E--> 757	gccatctcca	agctggcgtc	gctgagccca	tccggcgagg	tggacgcgct
E--> 758	210	220	230	240	250
E--> 759	cttcaccgac	ctcgtcacgg	cgtgcgtccc	ggcgagcccc	gtcgacgtgg
E--> 760	260	270	280	290	300
E--> 761	ccaaagctcg	cccgaggcg	caggcgatgc	gggaggagct	catccgcctc
E--> 762	310	320	330	340	350
E--> 763	tgctccgccc	ccgaggggcca	cctcgaggcg	cactacgccc	acatgctcgc
E--> 764	360	370	380	390	400
E--> 765	cgccttcgac	aaccgcgtcg	accacccgtc	ccgcttcccg	tactacggca
E--> 766	410	420	430	440	450
E--> 767	actacgtcaa	cctgagcaag	ctggagtagc	acccctctcg	ccgctacgtc
E--> 768	460	470	480	490	500
E--> 769	cccgccattg	cccccacccg	cgtgcgcctc	gtcgggtcgg	gcccgctgcc
E--> 770	510	520	530	540	550
E--> 771	gttcagctcc	ctcggtctcg	ctgcgcacca	cctgcccggac	gcgggtttcg
E--> 772	560	570	580	590	600
E--> 773	acaactacga	ccgggtgcggc	gcggccaaacg	agcggggcgag	gaggctgttc
E--> 774	610	620	630	640	650
E--> 775	cgcggcgccg	acgagggccct	cggcgccgcgc	atggcggttcc	acaccgcccga
E--> 776	660	670	680	690	700
E--> 777	cgtggcgacc	ctgacgggggg	agctcggcgc	gtacgacgtc	gtgttccctgg
E--> 778	710	720	730	740	750
E--> 779	cggcgctcg	gggcatggcg	gccgaggaga	aggccgggggt	gatcgcgacac
E--> 780	760	770	780	790	800
E--> 781	ctggcgccgc	acatggcgga	cggcgccggcg	ctcgctgtgc	ggacggcgca
E--> 782	810	820	830	840	850
E--> 783	cggggcgccgc	gggttcctgt	acccgatcgt	cgatcccggag	gacgtcaggc
E--> 784	860	870	880	890	900
E--> 785	gtggcggtt	cgacgttctg	gcgggtgtgcc	acccggagga	cgaggtgatc
E--> 786	910	920	930	940	950
E--> 787	aactccgtca	tcgtcgcccc	caaggtcggt	gccggccggcc	ccggccggccgc
E--> 788	960	970	980	990	1000
E--> 789	ggcgccaga	gacgagctcg	cggactcgcg	cgggcggttt	ctggcggtgg
E--> 790	1010	1020	1030	1040	1050
E--> 791	tcgggcccgc	gtccacgtgc	tgcaaggtgg	aggcgagcgc	ggttgagaag
E--> 792	1060	1070	1080	1090	1100
E--> 793	gcagaagagt	ttgcccggcaa	caaggagctg	tccgtctaaac	agccggacga
E--> 794	1110	1120	1130	1140	1150
E--> 795	tcgaaaggcg	cactatatta	tggcaataaa	tcattttgatt	atacttatgc
E--> 796	1160	1170	1180	1190	1200
E--> 797	tgcatttgcg	aagctaagg	atactatgca	agccatatgt	ttgtgttcgt
E--> 798	1210	1220	1230	1240	1250
E--> 799	acgtgttgtt	tgggacgtac	agttgttgg	ttgtacgtcg	tgaagtactg
E--> 800	1260	1270	1280	1290	1300
E--> 801	aagtgttcac	agtagatcac	aagttcacag	caatcaatga	ggaccctgt
E--> 802	1310	1320	1330	1340	1350
E--> 803	agccagtgt	aacgaggaac	atgcccattcg	tgtatgacag	tgagaaatta
E--> 804	1360	1370	1380		

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

E--> 805 tataagaaaa acatTTTgtg ac

808 <210> SEQ ID NO: 17

809 <211> LENGTH: 320

810 <212> TYPE: PRT

811 <213> ORGANISM: Arabidopsis thaliana

W--> 812 <400> SEQUENCE: 17

814 Met Ala Cys Gln Asn Asn Leu Val Val Lys Gln Ile Ile Asp Leu	15
815 Tyr Asp Gln Ile Ser Lys Leu Lys Ser Leu Lys Pro Ser Lys Asn	30
816 Val Asp Thr Leu Phe Gly Gln Leu Val Ser Thr Cys Leu Pro Thr	45
817 Asp Thr Asn Ile Asp Val Thr Asn Met Cys Glu Glu Val Lys Asp	60
818 Met Arg Ala Asn Leu Ile Lys Leu Cys Gly Glu Ala Glu Gly Tyr	75
819 Leu Glu Gln His Phe Ser Thr Ile Leu Gly Ser Leu Gln Glu Asp	90
820 Gln Asn Pro Leu Asp His Leu His Ile Phe Pro Tyr Tyr Ser Asn	105
821 Tyr Leu Lys Leu Gly Lys Leu Glu Phe Asp Leu Leu Ser Gln His	120
822 Ser Ser His Val Pro Thr Lys Ile Ala Phe Val Gly Ser Gly Pro	135
823 Met Pro Leu Thr Ser Ile Val Leu Ala Lys Phe His Leu Pro Asn	150
824 Thr Thr Phe His Asn Phe Asp Ile Asp Ser His Ala Asn Thr Leu	165
825 Ala Ser Asn Leu Val Ser Arg Asp Pro Asp Leu Ser Lys Arg Met	180
826 Ile Phe His Thr Thr Asp Val Leu Asn Ala Thr Glu Ala Leu Asp	195
827 Gln Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Asp Lys	210
828 Glu Ser Lys Val Lys Ala Ile Glu His Leu Glu Lys His Met Ala	225
829 Pro Gly Ala Val Leu Met Leu Arg Arg Ala His Ala Leu Arg Ala	240
830 Phe Leu Tyr Pro Ile Val Asp Ser Ser Asp Leu Lys Gly Phe Gln	255
831 Leu Leu Thr Ile Tyr His Pro Thr Asp Asp Val Val Asn Ser Val	270
832 Val Ile Ala Arg Lys Leu Gly Gly Pro Thr Thr Pro Gly Val Asn	285
833 Gly Thr Arg Gly Cys Met Phe Met Pro Cys Asn Cys Ser Lys Ile	300
834 His Ala Ile Met Asn Asn Arg Gly Lys Lys Asn Met Ile Glu Glu	315

E--> 835 Phe Ser Thr Ile Glu

861 <210> SEQ ID NO: 19

862 <211> LENGTH: 320

863 <212> TYPE: PRT

864 <213> ORGANISM: Arabidopsis thaliana

W--> 865 <400> SEQUENCE: 19

867 Met Ala Cys Gln Asn Asn Leu Val Val Lys Gln Ile Met Asp Leu	15
868 Tyr Asn Gln Ile Ser Asn Leu Glu Ser Leu Lys Pro Ser Lys Asn	30
869 Val Asp Thr Leu Phe Arg Gln Leu Val Ser Thr Cys Leu Pro Thr	45
870 Asp Thr Asn Ile Asp Val Thr Glu Ile His Asp Glu Lys Val Lys	60
871 Asp Met Arg Ser His Leu Ile Lys Leu Cys Gly Glu Ala Glu Gly	75
872 Tyr Leu Glu Gln His Phe Ser Ala Ile Leu Gly Ser Phe Glu Asp	90
873 Asn Pro Leu Asn His Leu His Ile Phe Pro Tyr Tyr Asn Asn Tyr	105
874 Leu Lys Leu Gly Lys Leu Glu Phe Asp Leu Leu Ser Gln His Thr	120
875 Thr His Val Pro Thr Lys Val Ala Phe Ile Gly Ser Gly Pro Met	135
876 Pro Leu Thr Ser Ile Val Leu Ala Lys Phe His Leu Pro Asn Thr	150
877 Thr Phe His Asn Phe Asp Ile Asp Ser His Ala Asn Thr Leu Ala	165
878 Ser Asn Leu Val Ser Arg Asp Ser Asp Leu Ser Lys Arg Met Ile	180
879 Phe His Thr Thr Asp Val Leu Asn Ala Lys Glu Gly Leu Asp Gln	195
880 Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Asp Lys Glu	210
881 Ser Lys Val Lys Ala Ile Glu His Leu Glu Lys His Met Ala Pro	225
882 Gly Ala Val Val Met Leu Arg Ser Ala His Gly Leu Arg Ala Phe	240

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

883	Leu	Tyr	Pro	Ile	Val	Asp	Ser	Cys	Asp	Leu	Lys	Gly	Phe	Glu	Val	255
884	Leu	Thr	Ile	Tyr	His	Pro	Ser	Asp	Asp	Val	Val	Asn	Ser	Val	Val	270
885	Ile	Ala	Arg	Lys	Leu	Gly	Gly	Ser	Asn	Gly	Ala	Arg	Gly	Ser	Gln	285
886	Ile	Gly	Arg	Cys	Val	Val	Met	Pro	Cys	Asn	Cys	Ser	Lys	Val	His	300
887	Ala	Ile	Leu	Asn	Asn	Arg	Gly	Met	Glu	Lys	Asn	Leu	Ile	Glu	Glu	315
E--> 888	Phe	Ser	Ala	Ile	Glu											<i>envald</i>
915	<210> SEQ ID NO: 21														320	
916	<211> LENGTH: 320															
917	<212> TYPE: PRT															
918	<213> ORGANISM: Arabidopsis thaliana															
W--> 919	<400>	SEQUENCE: 21														
921	Met	Gly	Cys	Gln	Asp	Glu	Gln	Leu	Val	Gln	Thr	Ile	Cys	Asp	Leu	15
922	Tyr	Glu	Lys	Ile	Ser	Lys	Leu	Glu	Ser	Leu	Lys	Pro	Ser	Glu	Asp	30
923	Val	Asn	Ile	Leu	Phe	Lys	Gln	Leu	Val	Ser	Thr	Cys	Ile	Pro	Pro	45
924	Asn	Pro	Asn	Ile	Asp	Val	Thr	Lys	Met	Cys	Asp	Arg	Val	Gln	Glu	60
925	Ile	Arg	Leu	Asn	Leu	Ile	Lys	Ile	Cys	Gly	Leu	Ala	Glu	Gly	His	75
926	Leu	Glu	Asn	His	Phe	Ser	Ser	Ile	Leu	Thr	Ser	Tyr	Gln	Asp	Asn	90
927	Pro	Leu	His	His	Leu	Asn	Ile	Phe	Pro	Tyr	Tyr	Asn	Asn	Tyr	Leu	105
928	Lys	Leu	Gly	Lys	Leu	Glu	Phe	Asp	Leu	Leu	Glu	Gln	Asn	Leu	Asn	120
929	Gly	Phe	Val	Pro	Lys	Ser	Val	Ala	Phe	Ile	Gly	Ser	Gly	Pro	Leu	135
930	Pro	Leu	Thr	Ser	Ile	Val	Leu	Ala	Ser	Phe	His	Leu	Lys	Asp	Thr	150
931	Ile	Phe	His	Asn	Phe	Asp	Ile	Asp	Pro	Ser	Ala	Asn	Ser	Leu	Ala	165
932	Ser	Leu	Leu	Val	Ser	Ser	Asp	Pro	Asp	Ile	Ser	Gln	Arg	Met	Phe	180
933	Phe	His	Thr	Val	Asp	Ile	Met	Asp	Val	Thr	Glu	Ser	Leu	Lys	Ser	195
934	Phe	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Asn	Lys	Glu	210
935	Glu	Lys	Val	Val	Ile	Glu	His	Leu	Gln	Lys	His	Met	Ala	Pro		225
936	Gly	Ala	Val	Leu	Met	Leu	Arg	Ser	Ala	His	Gly	Pro	Arg	Ala	Phe	240
937	Leu	Tyr	Pro	Ile	Val	Glu	Pro	Cys	Asp	Leu	Gln	Gly	Phe	Glu	Val	255
938	Leu	Ser	Ile	Tyr	His	Pro	Thr	Asp	Asp	Val	Ile	Asn	Ser	Val	Val	270
939	Ile	Ser	Lys	Lys	His	Pro	Val	Val	Ser	Ile	Gly	Asn	Val	Gly	Gly	285
940	Pro	Asn	Ser	Cys	Leu	Leu	Lys	Pro	Cys	Asn	Cys	Ser	Lys	Thr	His	300
941	Ala	Lys	Met	Asn	Lys	Asn	Met	Met	Ile	Glu	Glu	Phe	Gly	Ala	Arg	315
E--> 942	Glu	Glu	Gln	Leu	Ser										<i>envald</i>	320

*Please see sample Sequence Listing
(attached) for valid format*

FYI
Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

<110> Smith, John; Smithgene Inc.
 <120> Example of a Sequence Listing
 <130> 01-00001
 <140> PCT/EP98/00001
 <141> 1998-12-31
 <150> US 08/999,999
 <151> 1997-10-15
 <160> 4
 <170> PatentIn version 2.0
 <210> 1
 <211> 389
 <212> DNA
 <213> Paramecium sp.
 <220>
 <221> CDS
 <222> (279) . . . (389)
 <300>
 <301> Doc, Richard
 <302> Isolation and Characterization of a Gene Encoding a
 Protease from Paramecium sp.
 <303> Journal of Genes
 <304> 1
 <305> 4
 <306> 1-7
 <307> 1988-06-31
 <308> 123456
 <309> 1988-06-31
 <400> 1
 agc tgc tgc tgc attc ctgt gt cct ttt ctct ctgg gct tct cacc ctgt ct atc agat ct 60
 aggg agat g tctt gacc ct cct ctgc ct tgc agct tc cagg cagg ct ggcagg cagc 120
 tcat gtgg ca att gct gg ca gt gcc acagg ct ttt cag cc agg ct taggg tgg gtt cc gc 180
 cgc ggc ggc gg cgg ccc ct ct cgc gct cct c tcg cgc ct ct ct ctc gct ct cct ctg ctc 240

Appendix 3, page 2

ggacacctgatt aggtgagcag gaggaggggg cagttgc atg gtt tca atg ttc agc 296
Met Val Ser Met Phe Ser 1 5

ttg tct ttc aaa tgg cct gga ttt tgt ttg ttt gtt tgt ttg ttc caa 344
Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val Cys Leu Phe Cln 10 15 20

tgt ccc aaa gtc ctc ccc tgt cac tca tca ctg cag ccg aat ctt 389
Cys Pro Lys Val Leu Pro Cys His Ser Ser Leu Cln Pro Asn Leu 25 30 35

<210> 2

<211> 37

<212> PRT

<213> Paramecium sp.

<400> 2

Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu 1 5 10 15

Phe Val Cys Leu Phe Cln Cys Pro Lys Val Leu Pro Cys His Ser Ser 20 25 30

Leu Cln Pro Asn Leu 35

<210> 3

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3

Met Val Asn Leu Glu Pro Met His Thr Glu Ile 1 5 10

<210> 4

<400> 4

000

[Annex VIII follows]

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other~ Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M, when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOS	Count includes total number of SEQ ID NOS	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	O
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	O
<302>	Title		O
<303>	Journal		O
<304>	Volume		O
<305>	Issue		O
<306>	Pages		O
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	O
<308>	Database Accession Number	Accession number assigned by database including database name	O
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	O
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	O

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd.	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	CM

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/674, 337

DATE: 10/26/2001
TIME: 15:00:34

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:283 W: Missing Blank Line separator, <400> field identifier
L:39 M:252 E: No. of Seq. differs, <211>LENGTH:Input:328 Found:0 SEQ:1
L:46 M:283 W: Missing Blank Line separator, <400> field identifier
L:47 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:0 SEQ:2
M:254 Repeated in SeqNo=2
L:48 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=2
L:118 M:283 W: Missing Blank Line separator, <400> field identifier
L:142 M:252 E: No. of Seq. differs, <211>LENGTH:Input:335 Found:0 SEQ:3
L:149 M:283 W: Missing Blank Line separator, <400> field identifier
L:151 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:0 SEQ:4
M:254 Repeated in SeqNo=4
L:152 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=4
L:225 M:283 W: Missing Blank Line separator, <400> field identifier
L:249 M:252 E: No. of Seq. differs, <211>LENGTH:Input:335 Found:0 SEQ:5
L:256 M:283 W: Missing Blank Line separator, <400> field identifier
L:257 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:0 SEQ:6
M:254 Repeated in SeqNo=6
L:258 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=6
L:328 M:283 W: Missing Blank Line separator, <400> field identifier
L:351 M:252 E: No. of Seq. differs, <211>LENGTH:Input:329 Found:0 SEQ:7
L:357 M:283 W: Missing Blank Line separator, <400> field identifier
L:359 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:0 SEQ:8
M:254 Repeated in SeqNo=8
L:360 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=8
L:427 M:283 W: Missing Blank Line separator, <400> field identifier
L:447 M:252 E: No. of Seq. differs, <211>LENGTH:Input:282 Found:0 SEQ:9
L:453 M:283 W: Missing Blank Line separator, <400> field identifier
L:455 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:0 SEQ:10
M:254 Repeated in SeqNo=10
L:456 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=10
L:513 M:283 W: Missing Blank Line separator, <400> field identifier
L:536 M:252 E: No. of Seq. differs, <211>LENGTH:Input:328 Found:0 SEQ:11
L:543 M:283 W: Missing Blank Line separator, <400> field identifier
L:545 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:0 SEQ:12
M:254 Repeated in SeqNo=12
L:546 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=12
L:619 M:283 W: Missing Blank Line separator, <400> field identifier
L:642 M:252 E: No. of Seq. differs, <211>LENGTH:Input:329 Found:0 SEQ:13
L:650 M:283 W: Missing Blank Line separator, <400> field identifier
L:652 M:254 E: No. of Bases conflict, LENGTH:Input:50 Counted:0 SEQ:14

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:34

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

L:653 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
M:254 Repeated in SeqNo=14
L:653 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=14
L:715 M:283 W: Missing Blank Line separator, <400> field identifier
L:739 M:252 E: No. of Seq. differs, <211>LENGTH:Input:332 Found:0 SEQ:15
L:750 M:254 E: No. of Bases conflict, LENGTH:Input:50 Counted:0 SEQ:16
M:254 Repeated in SeqNo=16
L:751 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=16
L:812 M:283 W: Missing Blank Line separator, <400> field identifier
L:835 M:252 E: No. of Seq. differs, <211>LENGTH:Input:320 Found:0 SEQ:17
L:841 M:283 W: Missing Blank Line separator, <400> field identifier
L:843 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=18
L:865 M:283 W: Missing Blank Line separator, <400> field identifier
L:888 M:252 E: No. of Seq. differs, <211>LENGTH:Input:320 Found:0 SEQ:19
L:894 M:283 W: Missing Blank Line separator, <400> field identifier
L:897 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=20
L:919 M:283 W: Missing Blank Line separator, <400> field identifier
L:942 M:252 E: No. of Seq. differs, <211>LENGTH:Input:320 Found:0 SEQ:21
L:948 M:283 W: Missing Blank Line separator, <400> field identifier
L:950 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=22